

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/765,012ADATE: 09/15/98
TIME: 15:22:05

INPUT SET: S28654.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Wild, Hanno; Hanco, Rudolf; Dorschug, Michael;
5 Horlein, Hans-Dietrich; Beunink, Jurgen;
6 Apeler, Heiner; Wehlmann, Hermann; and Sebal, Walter
7
8 (ii) TITLE OF INVENTION: HIL-4 MUTANT PROTEINS USED AS
9 ANTAGONISTS OR PARTIAL AGONISTS OF
10 HUMAN INTERLEUKIN 4
11 (iii) NUMBER OF SEQUENCES: 20
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Sprung Kramer Schaefer & Briscoe
14 (B) STREET: 660 White Plains Road
15 (C) CITY: Tarrytown
16 (D) STATE: New York
17 (E) COUNTRY: USA
18 (F) ZIP: 10591-5144
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
21 (B) COMPUTER: Apple Macintosh
22 (C) OPERATING SYSTEM: System 7.5
23 (D) SOFTWARE: WordPerfect 3.5
24 (vi) CURRENT APPLICATION DATA:
25 (A) APPLICATION NUMBER: 08/765,012
26 (B) FILING DATE: 19-DEC-1996
27 (C) CLASSIFICATION:
28 (vii) PRIOR APPLICATION DATA:
29 (A) APPLICATION NUMBER: PCT/EP95/02358
30 (B) FILING DATE: 19-JUN-1995
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: DE 44 23 131
33 (B) FILING DATE: 01-JUL-1994
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Kurt G. Briscoe
36 (B) REGISTRATION NUMBER: 33,141
37 (C) REFERENCE/DOCKET NUMBER: BAYER 9776-KGB
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (914) 332-1700
40 (B) TELEFAX: (914) 332-1844
41
42
43 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 16 base pairs
46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49 (ii) MOLECULE TYPE: cDNA
50 (iii) HYPOTHETICAL: no
51 (iv) ANTI-SENSE: no
52 (vi) ORIGINAL SOURCE:
53 (C) INDIVIDUAL ISOLATE: synthetic
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55
56 CATGCACAAG TGCGAT

16

57
58
59 (2) INFORMATION FOR SEQ ID NO: 2:
60 (i) SEQUENCE CHARACTERISTICS:
61 (A) LENGTH: 12 base pairs
62 (B) TYPE: nucleic acid
63 (C) STRANDEDNESS: single
64 (D) TOPOLOGY: linear
65 (ii) MOLECULE TYPE: cDNA
66 (iii) HYPOTHETICAL: no
67 (iv) ANTI-SENSE: no
68 (vi) ORIGINAL SOURCE:
69 (C) INDIVIDUAL ISOLATE: synthetic
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

71
72 ATCGCACTTG TG

12

73
74 (2) INFORMATION FOR SEQ ID NO: 3:
75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 21 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80 (ii) MOLECULE TYPE: cDNA
81 (iii) HYPOTHETICAL: no
82 (iv) ANTI-SENSE: no
83 (vi) ORIGINAL SOURCE:
84 (C) INDIVIDUAL ISOLATE: synthetic
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

86
87 GCCTCCAAGG ACACAACTGA G

21

88
89 (2) INFORMATION FOR SEQ ID NO: 4:
90 (i) SEQUENCE CHARACTERISTICS:
91 (A) LENGTH: 24 base pairs
92 (B) TYPE: nucleic acid
93 (C) STRANDEDNESS: single
94 (D) TOPOLOGY: linear
95 (ii) MOLECULE TYPE: cDNA
96 (iii) HYPOTHETICAL: no
97 (iv) ANTI-SENSE: no
98 (vi) ORIGINAL SOURCE:
99 (C) INDIVIDUAL ISOLATE: synthetic

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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

101

102 GTGAAGGAAG CCGACCAGAG TACG

24

103

104 (2) INFORMATION FOR SEQ ID NO: 5:

105 (i) SEQUENCE CHARACTERISTICS:

106 (A) LENGTH: 36 base pairs

107 (B) TYPE: nucleic acid

108 (C) STRANDEDNESS: single

109 (D) TOPOLOGY: linear

110 (ii) MOLECULE TYPE: cDNA

111 (iii) HYPOTHETICAL: no

112 (iv) ANTI-SENSE: no

113 (vi) ORIGINAL SOURCE:

114 (C) INDIVIDUAL ISOLATE: synthetic

115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

116

117 CTGGAGACTG CCATGGCCCA CAAGTGCGAT ATCACC

36

118

119

120 (2) INFORMATION FOR SEQ ID NO: 6:

121 (i) SEQUENCE CHARACTERISTICS:

122 (A) LENGTH: 131 amino acids

123 (B) TYPE: amino acid

124 (D) TOPOLOGY: linear

125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

126

127

128 Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu

129

1

5

130

131 Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu

132

10

15

133

134 Gln Lys Thr Leu Cys Thr Glu Leu Thr Val

135

20

25

136

137 Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr

138

30

35

139

140 Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala

141

40

45

142

143 Thr Val Leu Arg Gln Phe Tyr Ser His His

144

50

55

145

146 Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr

147

60

65

148

149 Ala Gln Gln Phe His Arg His Lys Gln Leu

150

70

75

151

152 Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn

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153 80 85
154
155 Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
156 90 95
157
158 Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
159 100 105
160
161 Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
162 110 115
163
164 Met Arg Glu Lys Asp Ser Lys Cys Ser Ser
165 120 125
166
167
168 (2) INFORMATION FOR SEQ ID NO: 7:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 131 amino acids
171 (B) TYPE: amino acid
172 (D) TOPOLOGY: linear
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
174
175
176 Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu
177 1 5
178
179 Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu
180 10 15
181
182 Gln Lys Thr Leu Cys Thr Glu Leu Thr Val
183 20 25
184
185 Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr
186 30 35
187
188 Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala
189 40 45
190
191 Thr Val Leu Arg Gln Phe Tyr Ser His His
192 50 55
193
194 Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
195 60 65
196
197 Ala Gln Gln Phe His Arg His Lys Gln Leu
198 70 75
199
200 Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn
201 80 85
202
203 Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
204 90 95
205

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206 Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
207 100 105
208
209 Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
210 110 115
211
212 Met Asp Glu Lys Asp Ser Lys Cys Ser Ser
213 120 125
214
215
216 (2) INFORMATION FOR SEQ ID NO: 8:
217 (i) SEQUENCE CHARACTERISTICS:
218 (A) LENGTH: 131 amino acids
219 (B) TYPE: amino acid
220 (D) TOPOLOGY: linear
221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
222
223
224 Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu
225 1 5
226
227 Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu
228 10 15
229
230 Gln Lys Thr Leu Cys Thr Glu Leu Thr Val
231 20 25
232
233 Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr
234 30 35
235
236 Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala
237 40 45
238
239 Thr Val Leu Arg Gln Phe Tyr Ser His His
240 50 55
241
242 Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
243 60 65
244
245 Ala Gln Gln Phe His Arg His Lys Gln Leu
246 70 75
247
248 Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn
249 80 85
250
251 Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
252 90 95
253
254 Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
255 100 105
256
257 Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
258 110 115

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SEQUENCE VERIFICATION REPORT
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Original Text